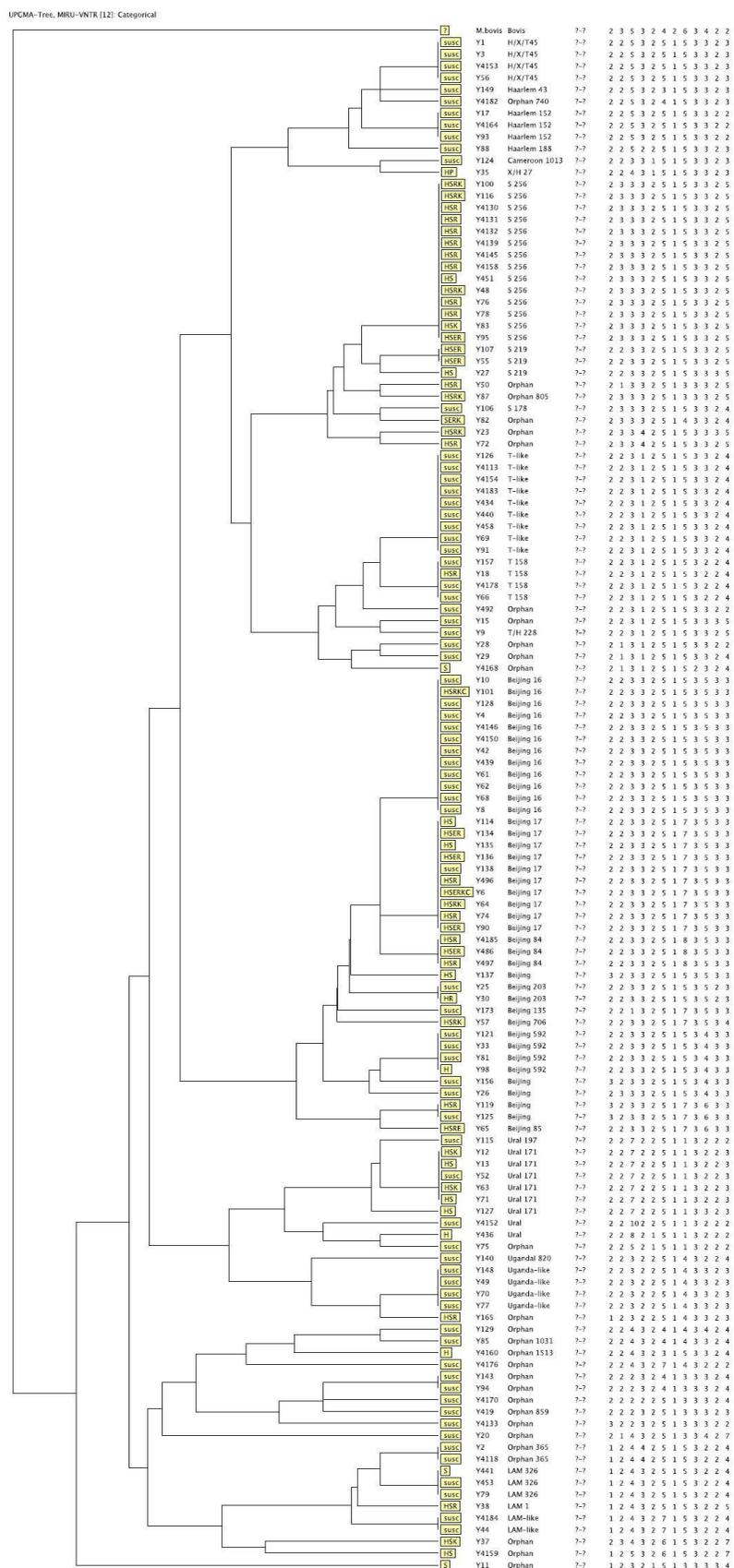


Primary Multidrug-Resistant *Mycobacterium tuberculosis* in 2 Regions, Eastern Siberia

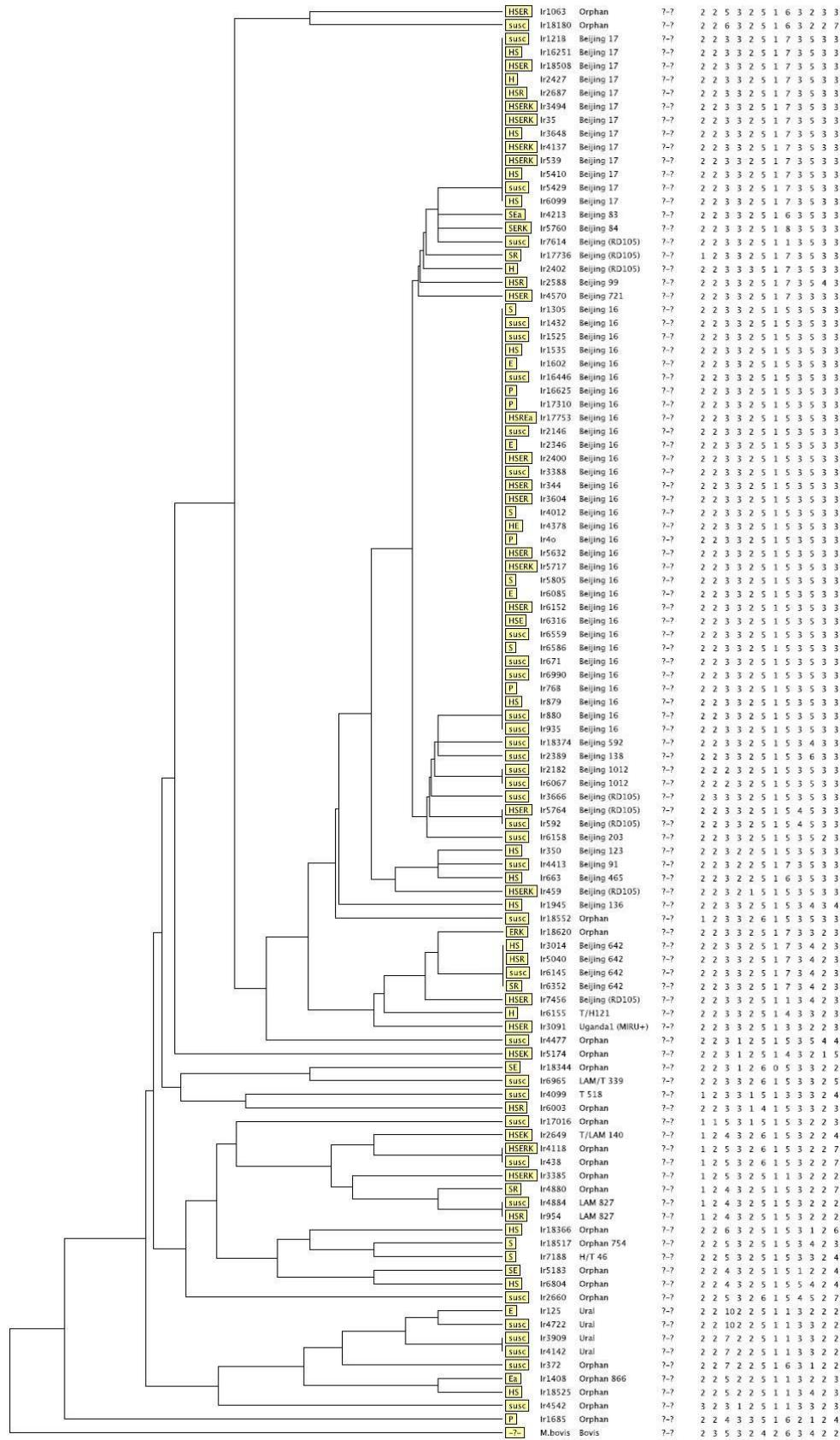
Technical Appendix



Technical Appendix Figure 1. Phylogenetic tree of *Mycobacterium tuberculosis* from 130 patients with primary tuberculosis, Yakutia, Russian Federation, determined by UPGMA (unweighted pair group method using arithmetic averages) tree by 12-loci mycobacterial interspersed repetitive unit–variable number tandem repeats (MIRU-VNTR). Yellow squares indicate drug resistance; H, isoniazid; S,

streptomycin; E, ethambutol; R, rifampin; K, kanamycin; C, capreomycin; susc, pansusceptible. Strain numbers are followed by lineage, VNTR international type number (if existing), and MIRU profile.

UPGMA-Tree, MIRU-VNTR [12]: Categorical



Technical Appendix Figure 2. Phylogenetic tree of *Mycobacterium tuberculosis* from 105 patients with primary tuberculosis, Irkutsk, Russian Federation, determined by UPGMA (unweighted pair group method using arithmetic averages) tree by 12-loci mycobacterial interspersed repetitive unit-variable number tandem repeats (MIRU-VNTR). Yellow squares indicate drug resistance; H, isoniazid; S, streptomycin; E, ethambutol; R, rifampin; K, kanamycin; C, capreomycin; susc, pansusceptible. Strain numbers are followed by lineage, VNTR international type number (if existing), and MIRU profile.